

## SEQUENCE LISTING FREE TEXT

dgoA CDS for KDPPGal Aldolase

dgoA CDS for KDPPGal Aldolase

dgoA CDS for KDPPGal Aldolase

aroB CDS for DHQ Synthase

tktA CDS for major Transketolase isozyme

tktB CDS for minor Transketolase isozyme

Primer JWF 430

Primer JWF 449

Primer JWF 484

Primer JWF 529

Primer JWF 501

Primer JWF 499

Primer JWF 541

Primer JWF 542

Primer JWF 610

Primer JWF 611

Primer JWF 625

Primer JWF 626

Primer JWF 541

Primer JWF 542

Primer JWF 636

Primer JWF 637

Primer JWF 669

Primer JWF 670

Primer JWF 599

Primer JWF 560

Primer JWF 484

Primer JWF 529

## SEQUENCE LISTING

<110> Board of Trustees operating Michigan State University  
Frost, John W.

<120> Methods and Materials for the Production of Shikimic Acid

<130> 6550-000086

<150> US 60/505,658

<151> 2003-09-24

<160> 34

<170> PatentIn version 3.3

<210> 1

<211> 618

<212> DNA

<213> Escherichia coli

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<221> CDS

<222> (1)..(615)

<223> dgoA CDS for KDPGal Aldolase

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acg ccc gac gag gcg ctg gcg cat gtt ggc gcg gtg att gac gcc ggg	96
Thr Pro Asp Glu Ala Leu Ala His Val Gly Ala Val Ile Asp Ala Gly	
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ttc gac gcg gtt gaa atc ccg ctg aat tcc cca caa tgg gag caa agc	144
Phe Asp Ala Val Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Gln Ser	
35 40 45	
att ccc gcc atc gtt gat gcg tac ggc gac aag gcg ttg att ggc gca	192
Ile Pro Ala Ile Val Asp Ala Tyr Gly Asp Lys Ala Leu Ile Gly Ala	
50 55 60	
ggg acg gta ctg aaa cct gaa cag gtc gat gcg ctc gcc agg atg ggc	240
Gly Thr Val Leu Lys Pro Glu Gln Val Asp Ala Leu Ala Arg Met Gly	
65 70 75 80	
tgt cag ctc atc gtt acg ccc aat atc cat agt gaa gtg atc cgc cgt	288
Cys Gln Leu Ile Val Thr Pro Asn Ile His Ser Glu Val Ile Arg Arg	
85 90 95	
gcg gtg ggc tac ggc atg acc gtc tgc ccc ggc tgc gcg acg gcg acc	336
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100 105 110	

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 Glu Ala Phe Thr Ala Leu Glu Ala Gly Ala Gln Ala Leu Lys Ile Phe  
 115 120 125  
 ccg tca tcg gct ttt ggt ccg caa tac atc aaa gcg tta aaa gcg gta 432  
 Pro Ser Ser Ala Phe Gly Pro Gln Tyr Ile Lys Ala Leu Lys Ala Val  
 130 135 140  
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 Leu Pro Ser Asp Ile Ala Val Phe Ala Val Gly Gly Val Thr Pro Glu  
 145 150 155 160  
 aac ctg gcg cag tgg ata gac gca ggt tgt gca ggg gcg ggc tta ggc 528  
 Asn Leu Ala Gln Trp Ile Asp Ala Gly Cys Ala Gly Ala Gly Leu Gly  
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 agc gat ctc tat cgc gcc ggg caa tcc gta gag cgc acc gcg cag cag 576  
 Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln  
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Phe Asp Ala Val Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Gln Ser  
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Ile Pro Ala Ile Val Asp Ala Tyr Gly Asp Lys Ala Leu Ile Gly Ala  
50 55 60

Gly Thr Val Leu Lys Pro Glu Gln Val Asp Ala Leu Ala Arg Met Gly  
65 70 75 80

Cys Gln Leu Ile Val Thr Pro Asn Ile His Ser Glu Val Ile Arg Arg  
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Ala Val Gly Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Thr  
100 105 110

Glu Ala Phe Thr Ala Leu Glu Ala Gly Ala Gln Ala Leu Lys Ile Phe  
115 120 125

Pro Ser Ser Ala Phe Gly Pro Gln Tyr Ile Lys Ala Leu Lys Ala Val  
130 135 140

Leu Pro Ser Asp Ile Ala Val Phe Ala Val Gly Gly Val Thr Pro Glu  
145 150 155 160

Asn Leu Ala Gln Trp Ile Asp Ala Gly Cys Ala Gly Ala Gly Leu Gly  
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180 185 190

Ala Ala Ala Phe Val Lys Ala Tyr Arg Glu Ala Val Gln  
195 200 205

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<223> dgoA CDS for KDPGal Aldolase

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Phe Asp Ala Val Glu Ile Pro Leu Asn Ser Pro Gln Trp Glu Lys Ser  
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Gly Thr Val Leu Gln Pro Glu Gln Val Asp Arg Leu Ala Ala Met Gly  
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 Cys Arg Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg Arg  
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 Glu Ala Phe Ser Ala Leu Asp Ala Gly Ala Gln Ala Leu Lys Ile Phe  
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 ccg tca tcg gct ttt ggc ccg gat tac atc aaa gcg ttg aaa gcc gtg 432  
 Pro Ser Ser Ala Phe Gly Pro Asp Tyr Ile Lys Ala Leu Lys Ala Val  
 130 135 140  
 ctg ccg ccc gag gtt ccg gtc ttt gcc gtt ggc ggc gtg acg ccg gaa 480  
 Leu Pro Pro Glu Val Pro Val Phe Ala Val Gly Gly Val Thr Pro Glu  
 145 150 155 160  
 aac ctg gcg cag tgg att aat gcc ggc tgt gtt ggg gca gga ttg ggt 528  
 Asn Leu Ala Gln Trp Ile Asn Ala Gly Cys Val Gly Ala Gly Leu Gly  
 165 170 175  
 agc gat ctc tat cgt gcc ggc cag tcg gtt gaa cgt acc gcg cag cag 576  
 Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln  
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 <213> *Klebsiella pneumoniae*

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35 40 45

Ile Pro Gln Val Val Asp Ala Tyr Gly Glu Gln Ala Leu Ile Gly Ala  
50 55 60

Gly Thr Val Leu Gln Pro Glu Gln Val Asp Arg Leu Ala Ala Met Gly  
65 70 75 80

Cys Arg Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg Arg  
85 90 95

Ala Val Gly Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Ser  
100 105 110

Glu Ala Phe Ser Ala Leu Asp Ala Gly Ala Gln Ala Leu Lys Ile Phe  
115 120 125

Pro Ser Ser Ala Phe Gly Pro Asp Tyr Ile Lys Ala Leu Lys Ala Val  
130 135 140

Leu Pro Pro Glu Val Pro Val Phe Ala Val Gly Gly Val Thr Pro Glu  
145 150 155 160

Asn Leu Ala Gln Trp Ile Asn Ala Gly Cys Val Gly Ala Gly Leu Gly  
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<223> dgoA CDS for KDPGal Aldolase

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 att tct tcc gtg gtg aag gcg tat ggc ggc agg gcg ctt att ggc gct 192  
 Ile Ser Ser Val Val Lys Ala Tyr Gly Gly Arg Ala Leu Ile Gly Ala  
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 Gly Thr Val Leu Lys Pro Glu Gln Val Asp Gln Leu Ala Gly Met Gly  
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 Cys Lys Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg  
 85 90 95  
 gcg gtg agc tat ggc atg acc gtg tgt ccg ggc tgc gcc acg gca acg 336  
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 130 135 140  
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 145 150 155 160  
 aac cta gcg caa tgg att aaa gca ggc tgt gtg ggc gcg gga ttg ggt 528  
 Asn Leu Ala Gln Trp Ile Lys Ala Gly Cys Val Gly Ala Gly Leu Gly  
 165 170 175  
 agc gat ctc tat cgc gcc ggg caa tcc gtt gaa cgc acc gcg cag cag 576  
 Ser Asp Leu Tyr Arg Ala Gly Gln Ser Val Glu Arg Thr Ala Gln Gln  
 180 185 190  
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 Ile Ser Ser Val Val Lys Ala Tyr Gly Gly Arg Ala Leu Ile Gly Ala  
 50 55 60  
 Gly Thr Val Leu Lys Pro Glu Gln Val Asp Gln Leu Ala Gly Met Gly  
 65 70 75 80  
 Cys Lys Leu Ile Val Thr Pro Asn Ile Gln Pro Glu Val Ile Arg Arg  
 85 90 95  
 Ala Val Ser Tyr Gly Met Thr Val Cys Pro Gly Cys Ala Thr Ala Thr  
 100 105 110  
 Glu Ala Phe Ser Ala Leu Asp Ala Gly Ala Gln Ala Leu Lys Ile Phe  
 115 120 125  
 Pro Ser Ser Ala Phe Gly Pro Gly Tyr Ile Ser Ala Leu Lys Ala Val  
 130 135 140  
 Leu Pro Pro Asp Val Pro Leu Phe Ala Val Gly Gly Val Thr Pro Glu  
 145 150 155 160  
 Asn Leu Ala Gln Trp Ile Lys Ala Gly Cys Val Gly Ala Gly Leu Gly  
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&lt;223&gt; aroB CDS for DHQ Synthase

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Ile Ala Ser Gly Leu Phe Asn Glu Pro Ala Ser Phe Leu Pro Leu Lys	
20 25 30	
tcg ggc gag cag gtc atg ttg gtc acc aac gaa acc ctg gct cct ctg	144
Ser Gly Glu Gln Val Met Leu Val Thr Asn Glu Thr Leu Ala Pro Leu	
35 40 45	
tat ctc gat aag gtc cgc ggc gta ctt gaa cag gcg ggt gtt aac gtc	192
Tyr Leu Asp Lys Val Arg Gly Val Leu Glu Gln Ala Gly Val Asn Val	
50 55 60	
gat agc gtt atc ctc cct gac ggc gag cag tat aaa agc ctg gct gta	240
Asp Ser Val Ile Leu Pro Asp Gly Glu Gln Tyr Lys Ser Leu Ala Val	
65 70 75 80	
ctc gat acc gtc ttt acg gcg ttg tta caa aaa ccg cat ggt cgc gat	288
Leu Asp Thr Val Phe Thr Ala Leu Leu Gln Lys Pro His Gly Arg Asp	
85 90 95	
act acg ctg gtg gcg ctt ggc ggc ggc gta gtg ggc gat ctg acc ggc	336
Thr Thr Leu Val Ala Leu Gly Gly Gly Val Val Gly Asp Leu Thr Gly	
100 105 110	
ttc gcg gcg gcg agt tat cag cgc ggt gtc cgt ttc att caa gtc ccg	384
Phe Ala Ala Ala Ser Tyr Gln Arg Gly Val Arg Phe Ile Gln Val Pro	
115 120 125	
acg acg tta ctg tcg cag gtc gat tcc tcc gtt ggc ggc aaa act gcg	432
Thr Thr Leu Leu Ser Gln Val Asp Ser Ser Val Gly Gly Lys Thr Ala	
130 135 140	
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Val Asn His Pro Leu Gly Lys Asn Met Ile Gly Ala Phe Tyr Gln Pro	
145 150 155 160	
gct tca gtg gtg gtg gat ctc gac tgt ctg aaa acg ctt ccc ccg cgt	528
Ala Ser Val Val Val Asp Leu Asp Cys Leu Lys Thr Leu Pro Pro Arg	
165 170 175	
gag tta gcg tcg ggg ctg gca gaa gtc atc aaa tac ggc att att ctt	576
Glu Leu Ala Ser Gly Leu Ala Glu Val Ile Lys Tyr Gly Ile Ile Leu	
180 185 190	
gac ggt gcg ttt ttt aac tgg ctg gaa gag aat ctg gat gcg ttg ttg	624
Asp Gly Ala Phe Phe Asn Trp Leu Glu Glu Asn Leu Asp Ala Leu Leu	
195 200 205	
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245                               250                               255

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260                               265                               270

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Val Met Ala Ala Arg Thr Ser Glu Arg Leu Gly Gln Phe Ser Ser Ala
275                               280                               285

gaa acg cag cgt att ata acc ctg ctc aag cgg gct ggg tta ccg gtc      912
Glu Thr Gln Arg Ile Ile Thr Leu Leu Lys Arg Ala Gly Leu Pro Val
290                               295                               300

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Asn Gly Pro Arg Glu Met Ser Ala Gln Ala Tyr Leu Pro His Met Leu
305                               310                               315                               320

cgt gac aag aaa gtc ctt gcg gga gag atg cgc tta att ctt ccg ttg      1008
Arg Asp Lys Lys Val Leu Ala Gly Glu Met Arg Leu Ile Leu Pro Leu
325                               330                               335

gca att ggt aag agt gaa gtt cgc agc ggc gtt tcg cac gag ctt gtt      1056
Ala Ile Gly Lys Ser Glu Val Arg Ser Gly Val Ser His Glu Leu Val
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35                               40                               45

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Asp Ser Val Ile Leu Pro Asp Gly Glu Gln Tyr Lys Ser Leu Ala Val  
 65 70 75 80

Leu Asp Thr Val Phe Thr Ala Leu Leu Gln Lys Pro His Gly Arg Asp  
 85 90 95

Thr Thr Leu Val Ala Leu Gly Gly Gly Val Val Gly Asp Leu Thr Gly  
 100 105 110

Phe Ala Ala Ala Ser Tyr Gln Arg Gly Val Arg Phe Ile Gln Val Pro  
 115 120 125

Thr Thr Leu Leu Ser Gln Val Asp Ser Ser Val Gly Gly Lys Thr Ala  
 130 135 140

Val Asn His Pro Leu Gly Lys Asn Met Ile Gly Ala Phe Tyr Gln Pro  
 145 150 155 160

Ala Ser Val Val Val Asp Leu Asp Cys Leu Lys Thr Leu Pro Pro Arg  
 165 170 175

Glu Leu Ala Ser Gly Leu Ala Glu Val Ile Lys Tyr Gly Ile Ile Leu  
 180 185 190

Asp Gly Ala Phe Phe Asn Trp Leu Glu Glu Asn Leu Asp Ala Leu Leu  
 195 200 205

Arg Leu Asp Gly Pro Ala Met Ala Tyr Cys Ile Arg Arg Cys Cys Glu  
 210 215 220

Leu Lys Ala Glu Val Val Ala Ala Asp Glu Arg Glu Thr Gly Leu Arg  
 225 230 235 240

Ala Leu Leu Asn Leu Gly His Thr Phe Gly His Ala Ile Glu Ala Glu  
 245 250 255

Met Gly Tyr Gly Asn Trp Leu His Gly Glu Ala Val Ala Ala Gly Met  
 260 265 270

Val Met Ala Ala Arg Thr Ser Glu Arg Leu Gly Gln Phe Ser Ser Ala  
275 280 285

Glu Thr Gln Arg Ile Ile Thr Leu Leu Lys Arg Ala Gly Leu Pro Val  
290 295 300

Asn Gly Pro Arg Glu Met Ser Ala Gln Ala Tyr Leu Pro His Met Leu  
305 310 315 320

Arg Asp Lys Lys Val Leu Ala Gly Glu Met Arg Leu Ile Leu Pro Leu  
325 330 335

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<220>  
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<222> (1)..(1989)  
<223> tktA CDS for major Tranketolase isozyme

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Asp Ala Val Gln Lys Ala Lys Ser Gly His Pro Gly Ala Pro Met Gly  
20 25 30  
atg gct gac att gcc gaa gtc ctg tgg cgt gat ttc ctg aaa cac aac 144  
Met Ala Asp Ile Ala Glu Val Leu Trp Arg Asp Phe Leu Lys His Asn  
35 40 45  
ccg cag aat ccg tcc tgg gct gac cgt gac cgc ttc gtg ctg tcc aac 192  
Pro Gln Asn Pro Ser Trp Ala Asp Arg Asp Arg Phe Val Leu Ser Asn  
50 55 60  
ggc cac ggc tcc atg ctg atc tac agc ctg ctg cac ctc acc ggt tac 240  
Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr  
65 70 75 80

gat ctg ccg atg gaa gaa ctg aaa aac ttc cgt cag ctg cac tct aaa Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys 85 90 95	288
act ccg ggt cac ccg gaa gtg ggt tac acc gct ggt gtg gaa acc acc Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr 100 105 110	336
acc ggt ccg ctg ggt cag ggt att gcc aac gca gtc ggt atg gcg att Thr Gly Pro Leu Gly Gln Gly Ile Ala Asn Ala Val Gly Met Ala Ile 115 120 125	384
gca gaa aaa acg ctg gcg gcg cag ttt aac cgt ccg ggc cac gac att Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile 130 135 140	432
gtc gac cac tac acc tac gcc ttc atg ggc gac ggc tgc atg atg gaa Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu 145 150 155 160	480
ggc atc tcc cac gaa gtt tgc tct ctg gcg ggt acg ctg aag ctg ggt Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly 165 170 175	528
aaa ctg att gca ttc tac gat gac aac ggt att tct atc gat ggt cac Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His 180 185 190	576
gtt gaa ggc tgg ttc acc gac gac acc gca atg cgt ttc gaa gct tac Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr 195 200 205	624
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gaa atc tat gct cag tgg gat gcg aaa gaa gca ggc cag gcg aaa gaa Glu Ile Tyr Ala Gln Trp Asp Ala Lys Glu Ala Gly Gln Ala Lys Glu 290 295 300	912
tcc gca tgg aac gag aaa ttc gct gct tac gcg aaa gct tat ccg cag	960

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305					310					315					320		
gaa	gcc	gct	gaa	ttt	acc	cgc	cgt	atg	aaa	ggc	gaa	atg	ccg	tct	gac		1008
Glu	Ala	Ala	Glu	Phe	Thr	Arg	Arg	Met	Lys	Gly	Glu	Met	Pro	Ser	Asp		
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ttc	gac	gct	aaa	gcg	aaa	gag	ttc	atc	gct	aaa	ctg	cag	gct	aat	ccg		1056
Phe	Asp	Ala	Lys	Ala	Lys	Glu	Phe	Ile	Ala	Lys	Leu	Gln	Ala	Asn	Pro		
			340					345					350				
gcg	aaa	atc	gcc	agc	cgt	aaa	gcg	tct	cag	aat	gct	atc	gaa	gcg	ttc		1104
Ala	Lys	Ile	Ala	Ser	Arg	Lys	Ala	Ser	Gln	Asn	Ala	Ile	Glu	Ala	Phe		
		355					360					365					
ggg	ccg	ctg	ttg	ccg	gaa	ttc	ctc	ggc	ggg	tct	gct	gac	ctg	gcg	ccg		1152
Gly	Pro	Leu	Leu	Pro	Glu	Phe	Leu	Gly	Gly	Ser	Ala	Asp	Leu	Ala	Pro		
	370					375					380						
tct	aac	ctg	acc	ctg	tgg	tct	ggg	tct	aaa	gca	atc	aac	gaa	gat	gct		1200
Ser	Asn	Leu	Thr	Leu	Trp	Ser	Gly	Ser	Lys	Ala	Ile	Asn	Glu	Asp	Ala		
385					390					395					400		
gcg	ggg	aac	tac	atc	cac	tac	ggg	gtt	cgc	gag	ttc	ggg	atg	acc	gcg		1248
Ala	Gly	Asn	Tyr	Ile	His	Tyr	Gly	Val	Arg	Glu	Phe	Gly	Met	Thr	Ala		
			405					410					415				
att	gct	aac	ggg	atc	tcc	ctg	cac	ggg	ggc	ttc	ctg	ccg	tac	acc	tcc		1296
Ile	Ala	Asn	Gly	Ile	Ser	Leu	His	Gly	Gly	Phe	Leu	Pro	Tyr	Thr	Ser		
			420					425					430				
acc	ttc	ctg	atg	ttc	gtg	gaa	tac	gca	cgt	aac	gcc	gta	cgt	atg	gct		1344
Thr	Phe	Leu	Met	Phe	Val	Glu	Tyr	Ala	Arg	Asn	Ala	Val	Arg	Met	Ala		
		435				440					445						
gcg	ctg	atg	aaa	cag	cgt	cag	gtg	atg	gtt	tac	acc	cac	gac	tcc	atc		1392
Ala	Leu	Met	Lys	Gln	Arg	Gln	Val	Met	Val	Tyr	Thr	His	Asp	Ser	Ile		
	450					455					460						
ggg	ctg	ggc	gaa	gac	ggg	ccg	act	cac	cag	ccg	gtt	gag	cag	gtc	gct		1440
Gly	Leu	Gly	Glu	Asp	Gly	Pro	Thr	His	Gln	Pro	Val	Glu	Gln	Val	Ala		
465					470				475						480		
tct	ctg	cgc	gta	acc	ccg	aac	atg	tct	aca	tgg	cgt	ccg	tgt	gac	cag		1488
Ser	Leu	Arg	Val	Thr	Pro	Asn	Met	Ser	Thr	Trp	Arg	Pro	Cys	Asp	Gln		
			485						490					495			
gtt	gaa	tcc	gcg	gtc	gcg	tgg	aaa	tac	ggg	gtt	gag	cgt	cag	gac	ggc		1536
Val	Glu	Ser	Ala	Val	Ala	Trp	Lys	Tyr	Gly	Val	Glu	Arg	Gln	Asp	Gly		
			500					505					510				
ccg	acc	gca	ctg	atc	ctc	tcc	cgt	cag	aac	ctg	gcg	cag	cag	gaa	cga		1584
Pro	Thr	Ala	Leu	Ile	Leu	Ser	Arg	Gln	Asn	Leu	Ala	Gln	Gln	Glu	Arg		
		515					520					525					
act	gaa	gag	caa	ctg	gca	aac	atc	gcg	cgc	ggg	ggg	tat	gtg	ctg	aaa		1632
Thr	Glu	Glu	Gln	Leu	Ala	Asn	Ile	Ala	Arg	Gly	Gly	Tyr	Val	Leu	Lys		

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gtt gaa ctg gct gtt gct gcc tac gaa aaa ctg act gcc gaa ggc gtg Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val 565 570 575			1728
aaa gcg cgc gtg gtg tcc atg tcg tct acc gac gca ttt gac aag cag Lys Ala Arg Val Val Ser Met Ser Ser Thr Asp Ala Phe Asp Lys Gln 580 585 590			1776
gat gct gct tac cgt gaa tcc gta ctg ccg aaa gcg gtt act gca cgc Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg 595 600 605			1824
gtt gct gta gaa gcg ggt att gct gac tac tgg tac aag tat gtt ggc Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly 610 615 620			1872
ctg aac ggt gct atc gtc ggt atg acc acc ttc ggt gaa tct gct ccg Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Glu Ser Ala Pro 625 630 635 640			1920
gca gag ctg ctg ttt gaa gag ttc ggc ttc act gtt gat aac gtt gtt Ala Glu Leu Leu Phe Glu Glu Phe Gly Phe Thr Val Asp Asn Val Val 645 650 655			1968
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Gly His Gly Ser Met Leu Ile Tyr Ser Leu Leu His Leu Thr Gly Tyr  
65 70 75 80

Asp Leu Pro Met Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys  
85 90 95

Thr Pro Gly His Pro Glu Val Gly Tyr Thr Ala Gly Val Glu Thr Thr  
100 105 110

Thr Gly Pro Leu Gly Gln Gly Ile Ala Asn Ala Val Gly Met Ala Ile  
115 120 125

Ala Glu Lys Thr Leu Ala Ala Gln Phe Asn Arg Pro Gly His Asp Ile  
130 135 140

Val Asp His Tyr Thr Tyr Ala Phe Met Gly Asp Gly Cys Met Met Glu  
145 150 155 160

Gly Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Lys Leu Gly  
165 170 175

Lys Leu Ile Ala Phe Tyr Asp Asp Asn Gly Ile Ser Ile Asp Gly His  
180 185 190

Val Glu Gly Trp Phe Thr Asp Asp Thr Ala Met Arg Phe Glu Ala Tyr  
195 200 205

Gly Trp His Val Ile Arg Asp Ile Asp Gly His Asp Ala Ala Ser Ile  
210 215 220

Lys Arg Ala Val Glu Glu Ala Arg Ala Val Thr Asp Lys Pro Ser Leu  
225 230 235 240

Leu Met Cys Lys Thr Ile Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly  
245 250 255

Thr His Asp Ser His Gly Ala Pro Leu Gly Asp Ala Glu Ile Ala Leu  
260 265 270

Thr Arg Glu Gln Leu Gly Trp Lys Tyr Ala Pro Phe Glu Ile Pro Ser  
275 280 285

Glu Ile Tyr Ala Gln Trp Asp Ala Lys Glu Ala Gly Gln Ala Lys Glu  
 290 295 300  
 Ser Ala Trp Asn Glu Lys Phe Ala Ala Tyr Ala Lys Ala Tyr Pro Gln  
 305 310 315 320  
 Glu Ala Ala Glu Phe Thr Arg Arg Met Lys Gly Glu Met Pro Ser Asp  
 325 330 335  
 Phe Asp Ala Lys Ala Lys Glu Phe Ile Ala Lys Leu Gln Ala Asn Pro  
 340 345 350  
 Ala Lys Ile Ala Ser Arg Lys Ala Ser Gln Asn Ala Ile Glu Ala Phe  
 355 360 365  
 Gly Pro Leu Leu Pro Glu Phe Leu Gly Gly Ser Ala Asp Leu Ala Pro  
 370 375 380  
 Ser Asn Leu Thr Leu Trp Ser Gly Ser Lys Ala Ile Asn Glu Asp Ala  
 385 390 395 400  
 Ala Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala  
 405 410 415  
 Ile Ala Asn Gly Ile Ser Leu His Gly Gly Phe Leu Pro Tyr Thr Ser  
 420 425 430  
 Thr Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Val Arg Met Ala  
 435 440 445  
 Ala Leu Met Lys Gln Arg Gln Val Met Val Tyr Thr His Asp Ser Ile  
 450 455 460  
 Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Gln Val Ala  
 465 470 475 480  
 Ser Leu Arg Val Thr Pro Asn Met Ser Thr Trp Arg Pro Cys Asp Gln  
 485 490 495  
 Val Glu Ser Ala Val Ala Trp Lys Tyr Gly Val Glu Arg Gln Asp Gly  
 500 505 510  
 Pro Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Gln Glu Arg

515                      520                      525  
 Thr Glu Glu Gln Leu Ala Asn Ile Ala Arg Gly Gly Tyr Val Leu Lys  
     530                      535                      540  
 Asp Cys Ala Gly Gln Pro Glu Leu Ile Phe Ile Ala Thr Gly Ser Glu  
     545                      550                      555                      560  
 Val Glu Leu Ala Val Ala Ala Tyr Glu Lys Leu Thr Ala Glu Gly Val  
                     565                      570                      575  
 Lys Ala Arg Val Val Ser Met Ser Ser Thr Asp Ala Phe Asp Lys Gln  
                     580                      585                      590  
 Asp Ala Ala Tyr Arg Glu Ser Val Leu Pro Lys Ala Val Thr Ala Arg  
                     595                      600                      605  
 Val Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly  
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 Leu Asn Gly Ala Ile Val Gly Met Thr Thr Phe Gly Glu Ser Ala Pro  
     625                      630                      635                      640  
 Ala Glu Leu Leu Phe Glu Glu Phe Gly Phe Thr Val Asp Asn Val Val  
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 Ala Lys Ala Lys Glu Leu Leu  
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 Met Ser Arg Lys Asp Leu Ala Asn Ala Ile Arg Ala Leu Ser Met Asp  
 1                      5                      10                      15  
 gcg gta caa aaa gcc aac tct ggt cat ccc ggc gcg ccg atg ggc atg                      96  
 Ala Val Gln Lys Ala Asn Ser Gly His Pro Gly Ala Pro Met Gly Met

20	25	30	
gct gat att gcc gaa gtg ctg tgg aac gat ttt ctt aaa cat aac cct Ala Asp Ile Ala Glu Val Leu Trp Asn Asp Phe Leu Lys His Asn Pro 35 40 45			144
acc gac cca acc tgg tat gat cgc gac cgc ttt att ctt tcc aac ggt Thr Asp Pro Thr Trp Tyr Asp Arg Asp Arg Phe Ile Leu Ser Asn Gly 50 55 60			192
cac gcg tcg atg ctg ctc tac agt ttg cta cat ctg acc ggt tac gac His Ala Ser Met Leu Leu Tyr Ser Leu Leu His Leu Thr Gly Tyr Asp 65 70 75 80			240
ctg ccg ctg gaa gaa ctg aag aac ttc cgt cag ttg cat tcg aaa acc Leu Pro Leu Glu Glu Leu Lys Asn Phe Arg Gln Leu His Ser Lys Thr 85 90 95			288
cca ggc cac ccg gag att ggc tat acg cca ggc gtt gaa acc acc acc Pro Gly His Pro Glu Ile Gly Tyr Thr Pro Gly Val Glu Thr Thr Thr 100 105 110			336
ggc ccg ctt gga caa ggt ttg gcg aac gcc gtc ggg ctg gcg ata gca Gly Pro Leu Gly Gln Gly Leu Ala Asn Ala Val Gly Leu Ala Ile Ala 115 120 125			384
gag cgt aca ctg gcg gcg cag ttt aac cag cca gac cat gag atc gtc Glu Arg Thr Leu Ala Ala Gln Phe Asn Gln Pro Asp His Glu Ile Val 130 135 140			432
gat cac ttc acc tat gtg ttt atg ggc gac ggc tgc ctg atg gaa ggt Asp His Phe Thr Tyr Val Phe Met Gly Asp Gly Cys Leu Met Glu Gly 145 150 155 160			480
att tcc cac gaa gtc tgt tcg ctg gca ggc acg ctg gga ctg ggc aag Ile Ser His Glu Val Cys Ser Leu Ala Gly Thr Leu Gly Leu Gly Lys 165 170 175			528
ctg att ggt ttt tac gat cac aac ggt att tcc atc gac ggt gaa aca Leu Ile Gly Phe Tyr Asp His Asn Gly Ile Ser Ile Asp Gly Glu Thr 180 185 190			576
gaa ggc tgg ttt acc gac gat acg gca aaa cgt ttt gaa gcc tat cac Glu Gly Trp Phe Thr Asp Asp Thr Ala Lys Arg Phe Glu Ala Tyr His 195 200 205			624
tgg cat gtg atc cat gaa atc gac ggt cac gat ccg cag gcg gtg aag Trp His Val Ile His Glu Ile Asp Gly His Asp Pro Gln Ala Val Lys 210 215 220			672
gaa gcg atc ctt gaa gcg caa agc gtg aaa gat aag ccg tcg ctg att Glu Ala Ile Leu Glu Ala Gln Ser Val Lys Asp Lys Pro Ser Leu Ile 225 230 235 240			720
atc tgc cgt acg gtg att ggc ttt ggt tcg ccg aat aaa gca ggt aag Ile Cys Arg Thr Val Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly Lys 245 250 255			768

gaa gag gcg cac ggc gca cca ctg ggg gaa gaa gaa gtg gcg ctg gca Glu Glu Ala His Gly Ala Pro Leu Gly Glu Glu Glu Val Ala Leu Ala 260 265 270	816
cgg caa aaa ctg ggc tgg cac cat ccg cca ttt gag atc cct aaa gag Arg Gln Lys Leu Gly Trp His His Pro Pro Phe Glu Ile Pro Lys Glu 275 280 285	864
att tat cac gcc tgg gat gcc cgt gaa aaa ggc gaa aaa gcg cag cag Ile Tyr His Ala Trp Asp Ala Arg Glu Lys Gly Glu Lys Ala Gln Gln 290 295 300	912
agc tgg aat gag aag ttt gcc gcc tat aaa aag gct cat ccg caa ctg Ser Trp Asn Glu Lys Phe Ala Ala Tyr Lys Lys Ala His Pro Gln Leu 305 310 315 320	960
gca gaa gag ttt acc cga cgg atg agc ggt ggt tta ccg aag gac tgg Ala Glu Glu Phe Thr Arg Arg Met Ser Gly Gly Leu Pro Lys Asp Trp 325 330 335	1008
gag aaa acg act cag aaa tat atc aat gag tta cag gca aat ccg gcg Glu Lys Thr Thr Gln Lys Tyr Ile Asn Glu Leu Gln Ala Asn Pro Ala 340 345 350	1056
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ccg atg ctg cct gag ttg ctc ggc ggt tcg gcg gat ctg gct ccc agc Pro Met Leu Pro Glu Leu Leu Gly Gly Ser Ala Asp Leu Ala Pro Ser 370 375 380	1152
aac ctg acc atc tgg aaa ggt tct gtt tcg ctg aag gaa gat cca gcg Asn Leu Thr Ile Trp Lys Gly Ser Val Ser Leu Lys Glu Asp Pro Ala 385 390 395 400	1200
ggc aac tac att cac tac ggg gtg cgt gaa ttt ggc atg acc gct atc Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala Ile 405 410 415	1248
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ttc ctg atg ttt gtt gaa tac gcc cgt aac gcc gcg ccg atg gcg gca Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Ala Arg Met Ala Ala 435 440 445	1344
ctg atg aaa gcg cgg cag att atg gtt tat acc cac gac tca att ggc Leu Met Lys Ala Arg Gln Ile Met Val Tyr Thr His Asp Ser Ile Gly 450 455 460	1392
ctg ggc gaa gat ggt ccg acg cac cag gct gtt gag caa ctg gcc agc Leu Gly Glu Asp Gly Pro Thr His Gln Ala Val Glu Gln Leu Ala Ser 465 470 475 480	1440

ctg cgc tta acg cca aat ttc agc acc tgg cga ccg tgc gat cag gtg	1488
Leu Arg Leu Thr Pro Asn Phe Ser Thr Trp Arg Pro Cys Asp Gln Val	
485 490 495	
gaa gcg gcg gtg ggc tgg aag ctg gcg gtt gag cgc cac aac gga ccg	1536
Glu Ala Ala Val Gly Trp Lys Leu Ala Val Glu Arg His Asn Gly Pro	
500 505 510	
acg gca ctg atc ctc tca agg cag aat ctg gcc cag gtg gaa cgt acg	1584
Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Val Glu Arg Thr	
515 520 525	
ccg gat cag gtt aaa gag att gct cgt ggc ggt tat gtg ctg aaa gac	1632
Pro Asp Gln Val Lys Glu Ile Ala Arg Gly Gly Tyr Val Leu Lys Asp	
530 535 540	
agc ggc ggt aag cca gat att att ctg att gcc acc ggt tca gag atg	1680
Ser Gly Gly Lys Pro Asp Ile Ile Leu Ile Ala Thr Gly Ser Glu Met	
545 550 555 560	
gaa att acc ctg caa gcg gca gag aaa tta gca gga gaa ggt cgc aat	1728
Glu Ile Thr Leu Gln Ala Ala Glu Lys Leu Ala Gly Glu Gly Arg Asn	
565 570 575	
gta cgc gta gtt tcc ctg ccc tcg acc gat att ttc gac gcc cag gat	1776
Val Arg Val Val Ser Leu Pro Ser Thr Asp Ile Phe Asp Ala Gln Asp	
580 585 590	
gag gaa tat cgg gag tcg gtg ttg cct tct aac gtt gcg gct cgc gtg	1824
Glu Glu Tyr Arg Glu Ser Val Leu Pro Ser Asn Val Ala Ala Arg Val	
595 600 605	
gcg gtg gaa gca ggt att gcc gat tac tgg tac aag tat gtt ggt ctg	1872
Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly Leu	
610 615 620	
aaa ggg gca att gtc ggg atg acg ggt tac ggg gaa tct gct ccg gcg	1920
Lys Gly Ala Ile Val Gly Met Thr Gly Tyr Gly Glu Ser Ala Pro Ala	
625 630 635 640	
gat aag ctg ttc ccg ttc ttt ggc ttt acc gcc gag aat att gtg gca	1968
Asp Lys Leu Phe Pro Phe Phe Gly Phe Thr Ala Glu Asn Ile Val Ala	
645 650 655	
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Lys Ala His Lys Val Leu Gly Val Lys Gly Ala	
660 665	

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&lt;211&gt; 667

&lt;212&gt; PRT

&lt;213&gt; Escherichia coli

&lt;400&gt; 12

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Ala Asp Ile Ala	Glu Val Leu Trp	Asn Asp Phe Leu	Lys His Asn Pro
35	40	45	
Thr Asp Pro Thr	Trp Tyr Asp Arg	Asp Arg Phe Ile	Leu Ser Asn Gly
50	55	60	
His Ala Ser Met	Leu Leu Tyr Ser	Leu Leu His Leu	Thr Gly Tyr Asp
65	70	75	80
Leu Pro Leu Glu	Glu Leu Lys Asn	Phe Arg Gln Leu	His Ser Lys Thr
85	90	95	
Pro Gly His Pro	Glu Ile Gly Tyr	Thr Pro Gly Val	Glu Thr Thr Thr
100	105	110	
Gly Pro Leu Gly	Gln Gly Leu Ala	Asn Ala Val Gly	Leu Ala Ile Ala
115	120	125	
Glu Arg Thr Leu	Ala Ala Gln Phe	Asn Gln Pro Asp	His Glu Ile Val
130	135	140	
Asp His Phe Thr	Tyr Val Phe Met	Gly Asp Gly Cys	Leu Met Glu Gly
145	150	155	160
Ile Ser His Glu	Val Cys Ser Leu	Ala Gly Thr Leu	Gly Leu Gly Lys
165	170	175	
Leu Ile Gly Phe	Tyr Asp His Asn	Gly Ile Ser Ile	Asp Gly Glu Thr
180	185	190	
Glu Gly Trp Phe	Thr Asp Asp Thr	Ala Lys Arg Phe	Glu Ala Tyr His
195	200	205	
Trp His Val Ile	His Glu Ile Asp	Gly His Asp Pro	Gln Ala Val Lys
210	215	220	
Glu Ala Ile Leu	Glu Ala Gln Ser	Val Lys Asp Lys	Pro Ser Leu Ile

225                      230                      235                      240  
 Ile Cys Arg Thr Val Ile Gly Phe Gly Ser Pro Asn Lys Ala Gly Lys  
                                  245                                   250                                   255  
 Glu Glu Ala His Gly Ala Pro Leu Gly Glu Glu Glu Val Ala Leu Ala  
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 Arg Gln Lys Leu Gly Trp His His Pro Pro Phe Glu Ile Pro Lys Glu  
                                  275                                   280                                   285  
 Ile Tyr His Ala Trp Asp Ala Arg Glu Lys Gly Glu Lys Ala Gln Gln  
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 Ser Trp Asn Glu Lys Phe Ala Ala Tyr Lys Lys Ala His Pro Gln Leu  
 305                                   310                                   315                                   320  
 Ala Glu Glu Phe Thr Arg Arg Met Ser Gly Gly Leu Pro Lys Asp Trp  
                                  325                                   330                                   335  
 Glu Lys Thr Thr Gln Lys Tyr Ile Asn Glu Leu Gln Ala Asn Pro Ala  
                                  340                                   345                                   350  
 Lys Ile Ala Thr Arg Lys Ala Ser Gln Asn Thr Leu Asn Ala Tyr Gly  
                                  355                                   360                                   365  
 Pro Met Leu Pro Glu Leu Leu Gly Gly Ser Ala Asp Leu Ala Pro Ser  
                                  370                                   375                                   380  
 Asn Leu Thr Ile Trp Lys Gly Ser Val Ser Leu Lys Glu Asp Pro Ala  
 385                                   390                                   395                                   400  
 Gly Asn Tyr Ile His Tyr Gly Val Arg Glu Phe Gly Met Thr Ala Ile  
                                  405                                   410                                   415  
 Ala Asn Gly Ile Ala His His Gly Gly Phe Val Pro Tyr Thr Ala Thr  
                                  420                                   425                                   430  
 Phe Leu Met Phe Val Glu Tyr Ala Arg Asn Ala Ala Arg Met Ala Ala  
                                  435                                   440                                   445  
 Leu Met Lys Ala Arg Gln Ile Met Val Tyr Thr His Asp Ser Ile Gly  
                                  450                                   455                                   460



Leu Gly Glu Asp Gly Pro Thr His Gln Ala Val Glu Gln Leu Ala Ser  
 465 470 475 480

Leu Arg Leu Thr Pro Asn Phe Ser Thr Trp Arg Pro Cys Asp Gln Val  
 485 490 495

Glu Ala Ala Val Gly Trp Lys Leu Ala Val Glu Arg His Asn Gly Pro  
 500 505 510

Thr Ala Leu Ile Leu Ser Arg Gln Asn Leu Ala Gln Val Glu Arg Thr  
 515 520 525

Pro Asp Gln Val Lys Glu Ile Ala Arg Gly Gly Tyr Val Leu Lys Asp  
 530 535 540

Ser Gly Gly Lys Pro Asp Ile Ile Leu Ile Ala Thr Gly Ser Glu Met  
 545 550 555 560

Glu Ile Thr Leu Gln Ala Ala Glu Lys Leu Ala Gly Glu Gly Arg Asn  
 565 570 575

Val Arg Val Val Ser Leu Pro Ser Thr Asp Ile Phe Asp Ala Gln Asp  
 580 585 590

Glu Glu Tyr Arg Glu Ser Val Leu Pro Ser Asn Val Ala Ala Arg Val  
 595 600 605

Ala Val Glu Ala Gly Ile Ala Asp Tyr Trp Tyr Lys Tyr Val Gly Leu  
 610 615 620

Lys Gly Ala Ile Val Gly Met Thr Gly Tyr Gly Glu Ser Ala Pro Ala  
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27

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26

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29

<210> 22  
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27

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22

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&lt;223&gt; Primer JWF 636

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tccgtactgc gcgtattgag a

21

&lt;210&gt; 28

&lt;211&gt; 20

&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Primer JWF 637

&lt;400&gt; 28

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&lt;212&gt; DNA

&lt;213&gt; Artificial

&lt;220&gt;

&lt;223&gt; Primer JWF 669

&lt;400&gt; 29

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20

&lt;210&gt; 30

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